```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-724-107.res made by tport on Mon 4 Oct 104 14:23:17-PST.

Query sequence being compared:US-10-063-724-107 (1-2397)
Number of sequences searched:                3
Number of scores above cutoff:               3

Results of the initial comparison of US-10-063-724-107 (1-2397) with:
    File : US09830328C.seq

100-
   -
   -
N  -
U 50-
M  -
B  -
E  -
R  -
   -
O  -
F 10-
   -
S  -
E  5-
Q  -
U  -
E  *-
N  -
C  -
E  -
S  0-
     |---|---|---|---|---|---|---|---|---|---|
SCORE 0 266 532 798 1064 1331 1597 1863 2129 2395
STDEV 0                           1            *

               PARAMETERS
Similarity matrix   Unitary      K-tuple          4
Mismatch penalty    1            Joining penalty  30
Gap penalty         5.00         Window size      500
Gap size penalty    0.33
Cutoff score        1
Randomization group 0

            SEARCH STATISTICS
              Mean    Median
Scores:       836     57        Standard Deviation
                                1349.85
Times:        CPU
              00:00:00.00       Total Elapsed
                                00:00:00.00

Number of residues:              6063
Number of sequences searched:    3
Number of scores above cutoff:   3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                    Init.  Opt.
Sequence Name    Description                         Length  Score  Score  Sig.  Frame
------------------------------------------------------------------------------------
           **** 1 standard deviation above mean ****
1. US-09-830-328C-4 Sequence 4, Application U        2768    2395   2395   1.15   0

1. US-10-063-724-107 (1-2397)
   US-09-830-328C-4 Sequence 4, Application US/09830328C

Initial Score      =  2395    Optimized Score =  2395    Significance =  1.15
Residue Identity   =   99%    Matches         =  2395    Mismatches   =     2
Gaps               =     0    Conservative Substitutions =    0

                          X          10        20
                          AGAGAAAGAAGAGCGTCTCCAGCT
                          ||||||||||||||||||||||||
TTTTTTTCTTTTTCCCAGAGGCGGCGGCGGCGGGGGGAGAGAAAGAAGAGCGTCTCCAGCT
320         330        340        350        360 X      370        380

          30        40        50        60        70        80        90
GAAGCCAATGCAGCCCTCCGGCTCTCCGCGGAAGAGTTCCCTGCCCGATGAGCCCGTGCGTCCCCG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GAAGCCAATGCAGCCCTCCGGCTCTCCGCGGAAGAGTTCCCTGCCCGATGAGCCCGTGCGTCCCCG
390        400        410        420        430        440        450

          100       110       120       130       140       150       160
ACTATCCCCAGGCGGCGTGGGGCACGGGGCCCAGCGATCGCTCGCCGTTTGCCCTTGGGAGTAGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTATCCCCAGGCGGCGTGGGGCACGGGGCCCAGCGATCGCTCGCCGTTTGCCCTTGGGAGTAGG
460        470        480        490        500        510        520

          170       180       190       200       210       220       230
ATGTGGTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCACAATGGCAGAGAAGAATTCCGTGAAGTGTCTGC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGTGGTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCACAATGGCAGAGAAGAATTCCGTGAAGTGTCTGC
530        540        550        560        570        580        590

     240       250       260       270       280       290       300       310
GCTGCCTGCTCACGGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCTGCCTGCTCACGGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
600        610        620        630        640        650        660        670

     320       330       340       350       360       370       380
TGAGGGACTACCTAAATAATGTTCCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTGACTT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAGGGACTACCTAAATAATGTTCCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTGACTT
680        690        700        710        720        730        740

     390       400       410       420       430       440       450
ACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTCCTTATCATTGTGGGATGTTAGGGATATT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTCCTTATCATTGTGGGATGTTAGGGATATT
750        760        770        780        790        800        810

     460       470       480       490       500       510       520
GTGGACGGTGAAAGAAATCGTTGCTTCTTGCATGGTACTTGGAAGTTTGCTTGTCATTTTCTGTGTAG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTGGACGGTGAAAGAAATCGTTGCTTCTTGCATGGTACTTGGAAGTTTGCTTGTCATTTTCTGTGTAG
820        830        840        850        860        870        880

     530       540       550       560       570       580       590
AACTGGCTTGTGGCGTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACTGGCTTGTGGCGTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTT
890        900        910        920        930        940        950

     600       610       620       630       640       650       660       670
TGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGA
960        970        980        990        1000       1010       1020       1030
```

```
                  1540      1550      1560      1570      1580      1590      1600
         TTAGAAAATACTAATAACTTTTATTACTTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTAGAAAATACTAATAACTTTTATTACTTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAA
                  1900      1910      1920      1930      1940      1950      1960

                  1610      1620      1630      1640      1650      1660      1670
         ACTTTCAATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACTTAAAAGAGAGC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ACTTTCAATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACTTAAAAGAGAGC
                  1970      1980      1990      2000      2010      2020      2030

                  1680      1690      1700      1710      1720      1730      1740  1750
         AAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTCGTGTTAAATCTTGTATAATTCAG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTCGTGTTAAATCTTGTATAATTCAG
                  2040      2050      2060      2070      2080      2090      2100  2110

                  1760      1770      1780      1790      1800      1810      1820
         TCGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTAT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TCGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTAT
                  2120      2130      2140      2150      2160      2170      2180

                  1830      1840      1850      1860      1870      1880      1890
         TTTTAGCCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGCTTATATTACACATATAAACTGTTATTTA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTTTAGCCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGCTTATATTACACATATAAACTGTTATTTA
                  2190      2200      2210      2220      2230      2240      2250

                  1900      1910      1920      1930      1940      1950      1960
         AATACTTAACCACTAATTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AATACTTAACCACTAATTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTC
                  2260      2270      2280      2290      2300      2310      2320

                  1970      1980      1990      2000      2010      2020      2030
         TTTTAGGAGTATTAATAAGAAAATTTGCACATAACCTAGTTGATTCAGAAGGACTTGTATGCTGTGTTTTCT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTTTAGGAGTATTAATAAGAAAATTTGCACATAACCTAGTTGATTCAGAAGGACTTGTATGCTGTGTTTTCT
                  2330      2340      2350      2360      2370      2380      2390

                  2040      2050      2060      2070      2080      2090      2100  2110
         CCCAAATGAAGACTCTTTTGCACCTAAACACTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCCAAATGAAGACTCTTTTGCACCTAAACACTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAAGC
                  2400      2410      2420      2430      2440      2450      2460  2470

                  2120      2130      2140      2150      2160      2170      2180
         AATAGTCTCCAAGTCAATTAAATTCTACAGAAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAAT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AATAGTCTCCAAGTCAATTAAATTCTACAGAAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAAT
                  2480      2490      2500      2510      2520      2530      2540

                  2190      2200      2210      2220      2230      2240      2250
         CATTAAAACATGTGACAATTTAGAGATTCTTTGTTTATTTCACTGATTAATAATACTGTGGCAAATTACACA
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CATTAAAACATGTGACAATTTAGAGATTCTTTGTTTATTTCACTGATTAATAATACTGTGGCAAATTACACA
                  2550      2560      2570      2580      2590      2600      2610

                  2260      2270      2280      2290      2300      2310      2320
         GATTATTAAATTTTTTACAAGAGTATATTATTTATTTGAAAATGGGAAAAGTGCATTTTACTGTATTTTG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GATTATTAAATTTTTTACAAGAGTATATTATTTATTTGAAAATGGGAAAAGTGCATTTTACTGTATTTTG
                  2620      2630      2640      2650      2660      2670      2680

                  2330      2340      2350      2360      2370      2380      2390
         TGTATTTGTTTATTTCTTCAGAATATGCAGATAAAGAAAAATTAAAATGTGTCAATAAAATAATTTTCTAGAGAGTAA  X
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TGTATTTGTTTATTTCTTCAGAATATGCAGATAAAGAAAAATTAAAATGTGTCAATAAAATAATTTTCTAGAGAGTAA  X
                  2690      2700      2710      2720      2730      2740      2750

AAAAAAAAA
```

```
                  680       690       700       710       720       730       740
         GAGAGTTTAAGTGCTGTGTGGAGTAGTATATTTCACTGATATTTCACTGATATTTGGAAATGACAGAGATGGACTGGCCCCCAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GAGAGTTTAAGTGCTGTGTGGAGTAGTATATTTCACTGATATTTCACTGATATTTGGAAATGACAGAGATGGACTGGCCCCCAG
                  1040      1050      1060      1070      1080      1090      1100

                  750       760       770       780       790       800       810
         ATTCCTCGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATTCCTCGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATC
                  1110      1120      1130      1140      1150      1160      1170

                  820       830       840       850       860       870       880
         AAGAGGGTTGTGGGAGAGAAATGTATTCCTTTTGAGAGGAACCAAAACAACTGCAGGTGCTGAGGTTTCTGG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AAGAGGGTTGTGGGAGAGAAATGTATTCCTTTTGAGAGGAACCAAAACAACTGCAGGTGCTGAGGTTTCTGG
                  1180      1190      1200      1210      1220      1230      1240

                  890       900       910       920       930       940       950
         GAATCTTCCATTGGGGTGACACAAATCCTGGCCATGAATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GAATCTTCCATTGGGGTGACACAAATCCTGGCCATGAATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG
                  1250      1260      1270      1280      1290      1300      1310

                  960       970       980       990       1000      1010      1020  1030
         ATAGAAGGGAGGCCTGGGACGACCAGACCAAATGATGTCCTTGAAGAATGACAACTCCTCAGCACCTGTCATGTCCCT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATAGAAGGGAGGCCTGGGACGACCAGACCAAATGATGTCCTTGAAGAATGACAACTCCTCAGCACCTGTCATGTCCCT
                  1320      1330      1340      1350      1360      1370      1380  1390

                  1040      1050      1060      1070      1080      1090      1100
         CAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTGACACACATCCATGCAAACAGCTTAATACAC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTGACACACATCCATGCAAACAGCTTAATACAC
                  1400      1410      1420      1430      1440      1450      1460

                  1110      1120      1130      1140      1150      1160      1170
         ACTTTGAGATGGAGGAGTTATAAAAGAAATGTCACAGAAGAAAACCACAAAACTTGTTTTATTGGACTTGTG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ACTTTGAGATGGAGGAGTTATAAAAGAAATGTCACAGAAGAAAACCACAAAACTTGTTTTATTGGACTTGTG
                  1470      1480      1490      1500      1510      1520      1530

                  1180      1190      1200      1210      1220      1230      1240
         AATTTTGAGTACATACTATGTGTTCAGAAATATGTAGAAATAAAAAATGTGCCATAAAAATAACACCTAAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AATTTTGAGTACATACTATGTGTTCAGAAATATGTAGAAATAAAAAATGTGCCATAAAAATAACACCTAAG
                  1540      1550      1560      1570      1580      1590      1600

                  1250      1260      1270      1280      1290      1300      1310
         CATATTACTATTCTATGCTTATGTTTAAAATGAGGATGGGGAAAAGTTCATGTCATAAGTCACCACCTGGACAATAATT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CATATTACTATTCTATGCTTATGTTTAAAATGAGGATGGGGAAAAGTTCATGTCATAAGTCACCACCTGGACAATAATT
                  1610      1620      1630      1640      1650      1660      1670

                  1320      1330      1340      1350      1360      1370      1380  1390
         GATGCCCTTAAAATGCTGAAGACAGACGATGTCATACCCACTGTGTAGCCTGTAGCCTGTGTAGCTTTACTGAACACAG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GATGCCCTTAAAATGCTGAAGACAGACGATGTCATACCCACTGTGTAGCCTGTAGCCTGTGTAGCTTTACTGAACACAG
                  1680      1690      1700      1710      1720      1730      1740  1750

                  1400      1410      1420      1430      1440      1450      1460
         TTATGTTTTGAGGCAGCAGCATGTTTGATTAGGCATTTCCGCATCCAAATTCCGCATCCATGCAAACGAGTCACATATGTGGGACTG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTATGTTTTGAGGCAGCAGCATGTTTGATTAGGCATTTCCGCATCCAAATTCCGCATCCATGCAAACGAGTCACATATGTGGGACTG
                  1760      1770      1780      1790      1800      1810      1820

                  1470      1480      1490      1500      1510      1520      1530
         GAGCCATAGTAAAGGTTGATTTACTTCCTCCACCAACTAGTATATAAAGTACTAATTAAAGTGTAAGCTAACATAGGAAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GAGCCATAGTAAAGGTTGATTTACTTCCTCCACCAACTAGTATATAAAGTACTAATTAAAGTGTCAATTAAATGCTAACATAGGAAG
                  1830      1840      1850      1860      1870      1880      1890
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq1382andSeq4.res made by tport on Wed 15 Sep 104 14:43:39-PST.

Query sequence being compared:us100407391382 (1-442)
Number of sequences searched:        3
Number of scores above cutoff:       3

Results of the initial comparison of us100407391382 (1-442) with:
          File : US09830328C.seq
```

```
100-

N
U  50-
M
B
E
R
                                              *
O
F  10-
S
E
Q  5-
U
E
N
C
E  **                                         *
S   0-|----|----|----|----|----|----|----|----|
      46   92  138  184  231  277  323  369  415
SCORE 0
STDEV 0
```

```
              PARAMETERS

Similarity matrix   Unitary
Mismatch penalty    1          K-tuple            4
Gap penalty         5.00       Joining penalty    30
Gap size penalty    0.33       Window size        442
Cutoff score        1
Randomization group 0

              SEARCH STATISTICS

          Mean    Median    Standard Deviation
Scores:   159     29        221.72

          CPU                Total Elapsed
Times:    00:00:00.00        00:00:00.00

Number of residues:            6063
Number of sequences searched:  3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                   Init.  Opt.
Sequence Name    Description                Length  Score  Score  Sig.  Frame
-------------------------------------------------------------------------------
                 **** 1 standard deviation above mean ****
1. US-09-830-328C-4 Sequence 4, Application U  2768   415    419   1.15    0

1. us100407391382 (1-442)
   US-09-830-328C-4 Sequence 4, Application US/09830328C

Initial Score    = 415   Optimized Score       = 419   Significance = 1.15
Residue Identity = 96%   Matches               = 425   Mismatches   = 13
Gaps             =  4    Conservative Substitutions     = 0

             X        10        20
          GAATTCGGCCAAAGAGAGGCCTAG
          GGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAG----AG
970      980      990     1000     1010     1020     1030

          30        40        50        60        70        80        90
          TTTAAGTGCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAATTCC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TTTAAGTGCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAATTCC
1040     1050     1060     1070     1080     1090     1100

          100       110       120       130       140       150       160
          TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
1110     1120     1130     1140     1150     1160     1170     1180

          170       180       190       200       210       220       230
          GGTTGTGGGAGAAAATGTATTCCTTTTGAGGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GGTTGTGGGAGAAAATGTATTCCTTTTGAGGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATC
1190     1200     1210     1220     1230     1240     1250

          240       250       260       270       280       290       300       310
          TCCATTGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCCTGGGCTCTGTATTATGATAGA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TCCATTGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCCTGGGCTCTGTATTATGATAGA
1260     1270     1280     1290     1300     1310     1320

          320       330       340       350       360       370       380
          AGGGAGCCTGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCCAGCACCTGTCATGTCCTCAGTA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          AGGGAGCCGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCCAGCACCTGTCATGTCCTCAGTA
1330     1340     1350     1360     1370     1380     1390

          390       400       410       420       430       440  X
          GAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACCTGCAG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACCTGCAG
1400     1410     1420     1430     1440     1450     1460

          GAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAA
1470     1480     1490     1500
```

us-10-063-724-107.res
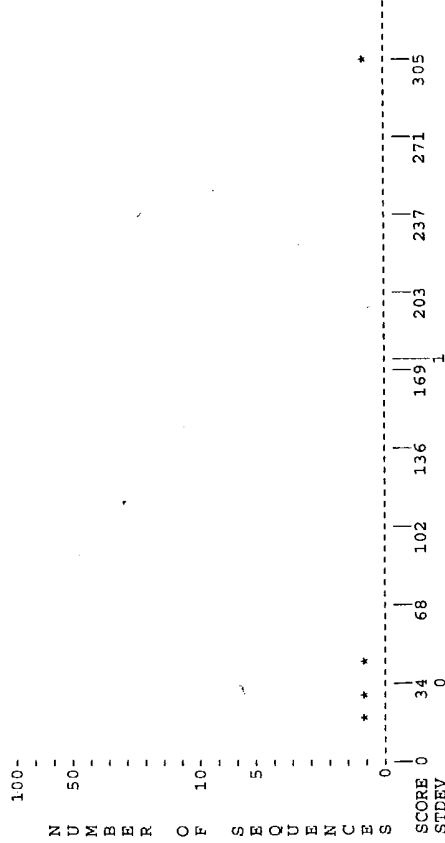
2760

```
> o <
o||o   IntelliGenetics
> o <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-724-108.res made by tport on Mon 4 Oct 104 14:27:06-PST.

Query sequence being compared:US-10-063-724-108 (1-305)
Number of sequences searched:        4
Number of scores above cutoff:       4

Results of the initial comparison of US-10-063-724-108 (1-305) with:
     File : US09830328C.pep
```

```
X                                                                            70
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMIAVCC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMIAVCC
X        10        20        30        40        50        60        70

                                                                            140
FLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVTLKARMTNYGLPRYR
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
FLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVTLKARMTNYGLPRYR
        80        90        100       110       120       130       140

                                                                            210
WLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
WLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG
        150       160       170       180       190       200       210

                                                                            280
TKQLQVLRFLGISIGVTQILAMLTITLLWALYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFE
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TKQLQVLRFLGISIGVTQILAMLTITLLWALYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFE
        220       230       240       250       260       270       280

290                 X
HTSMANSFNTHFEMEEL
|||||||||||||||||
HTSMANSFNTHFEMEEL
290                 X
```

```
    100-

         N
    50-  U
         M
         B
         E
         R

         O
    10-  F

         S
     5-  E
         Q
         U
         E
         N
         C
     0-  E  *        *                                                    *
         S
           -------|-------|-------|-------|-------|-------|-------|-------|
   SCORE 0     34    68    102   136   169   203   237   271   305
   STDEV 0      0                       1
```

```
                  PARAMETERS

Similarity matrix     PAM-150     K-tuple                1
Threshold level of sim.  16%
Mismatch penalty        1          Joining penalty       20
Gap penalty          5.00          Window size           305
Gap size penalty     0.05
Cutoff score            1
Randomization group     0

                  SEARCH STATISTICS

Scores:          Mean       Median      Standard Deviation
                 101         33            136.13

Times:           CPU                      Total Elapsed
            00:00:00.00                   00:00:00.00

Number of residues:              1078
Number of sequences searched:       4
Number of scores above cutoff:      4


1. US-10-063-724-108 (1-305)
   US-09-830-328C-2 Sequence 2, Application US/09830328C

Initial Score   =    305   Optimized Score   =    305   Significance =   1.50
Residue Identity = 100%    Matches           =    305   Mismatches   =     0
Gaps            =      0   Conservative Substitutions =    0
```